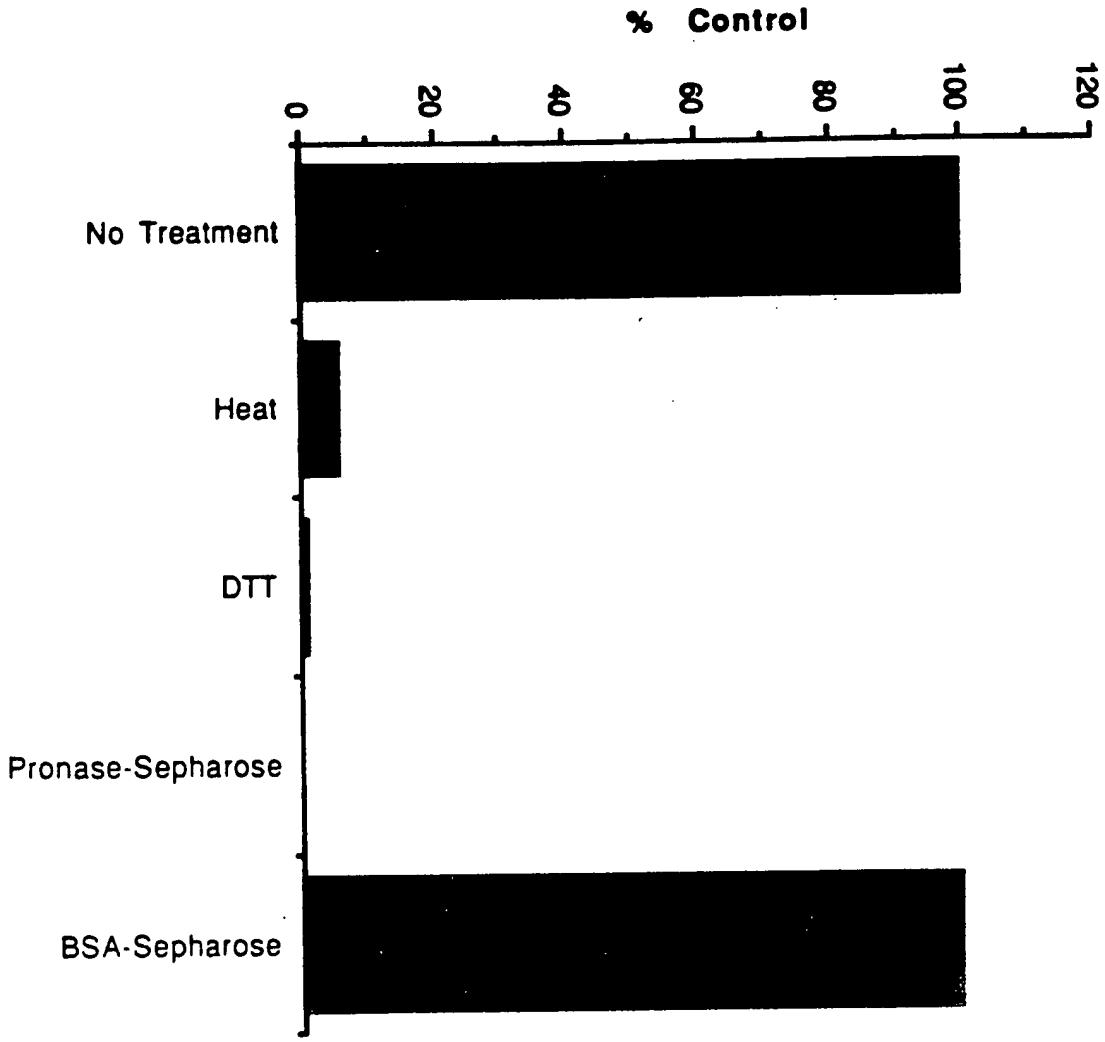

% Control
0
20
40
60
80
100
120
No Treatment
Heat
DTT
Pronase-Sepharose
BSA-Sepharose

Figure 1

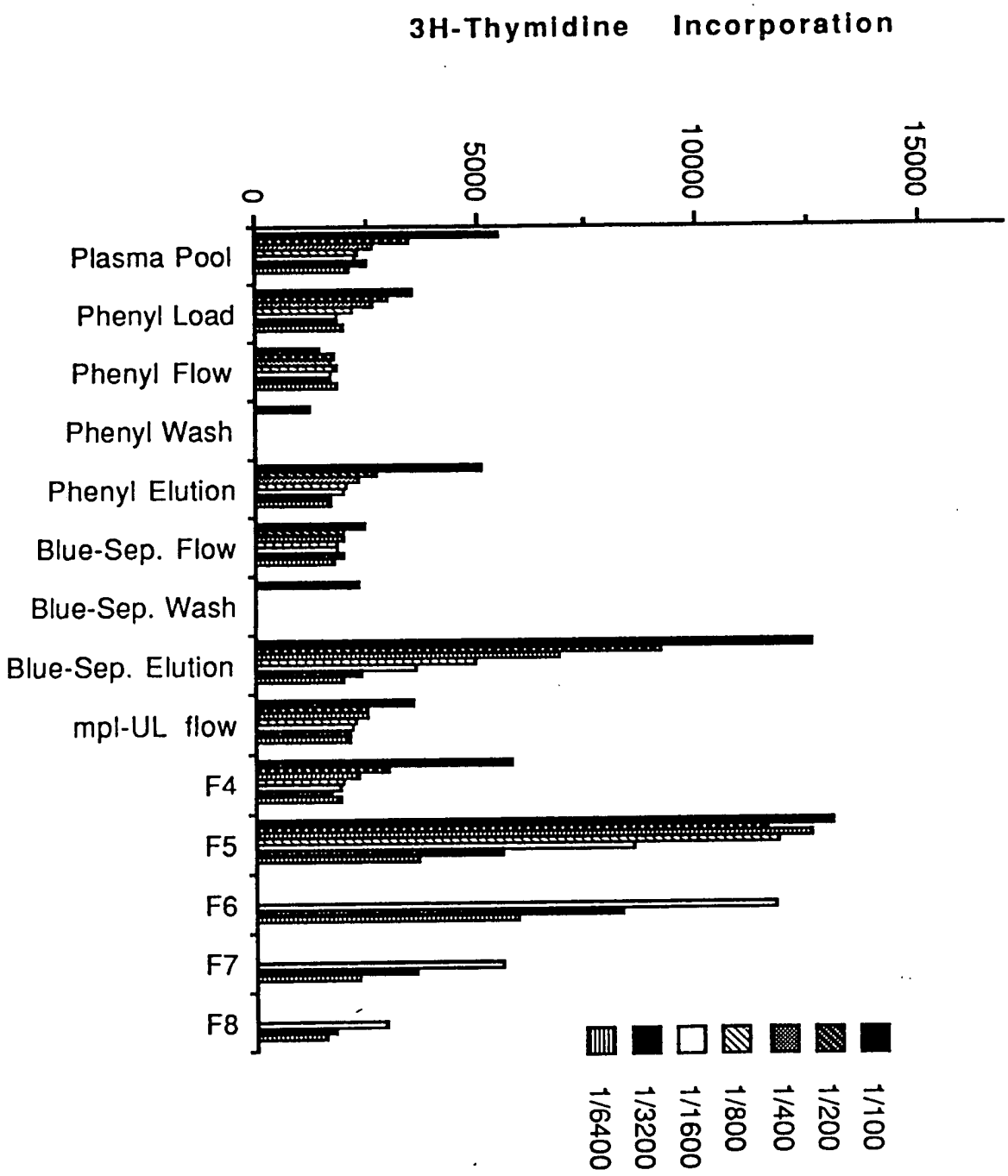

3H-Thymidine Incorporation
0
5000
10000
15000
Plasma Pool
Phenyl Load
Phenyl Flow
Phenyl Wash
Phenyl Elution
Blue-Sep. Flow
Blue-Sep. Wash
Blue-Sep. Elution
mpl-UL flow
F4
F5
F6
F7
F8
1/6400
1/3200
1/1600
1/800
1/400
1/200
1/100

Figure 2

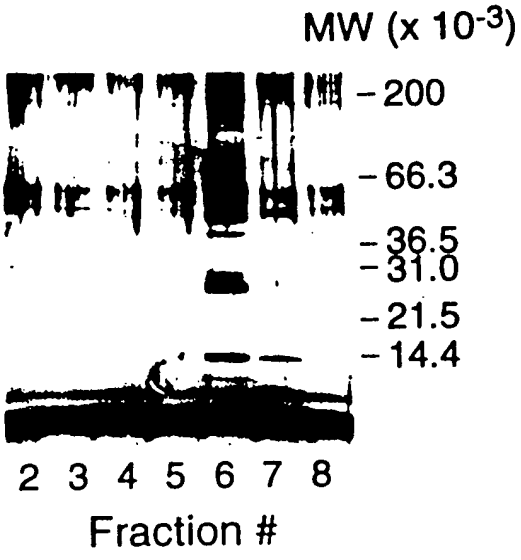


Figure 3

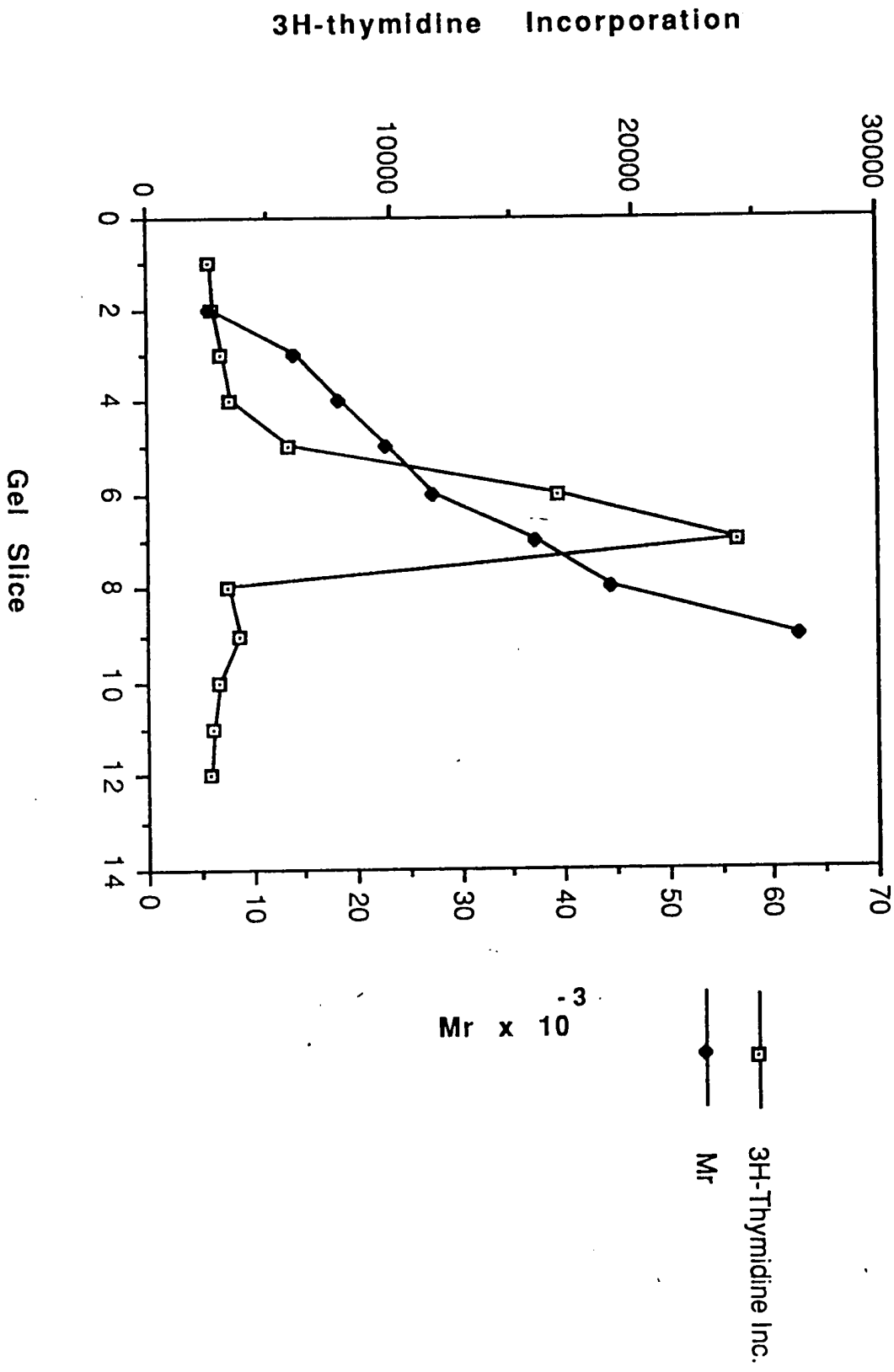

3H-thymidine Incorporation
Gel Slice
Mr x 10 -3
3H-Thymidine Inc.
Mr

Figure 4

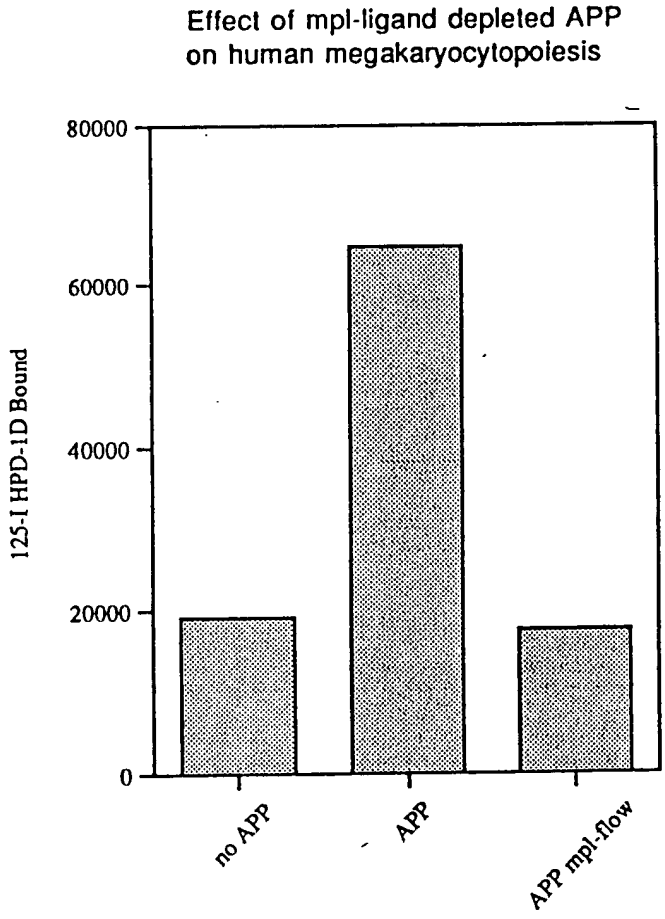

Effect of mpl-ligand depleted APP
on human megakaryocytopoiesis
125-I HPD-1D Bound
80000
60000
40000
20000
0
no APP
APP
APP mpl-flow

Figure 5

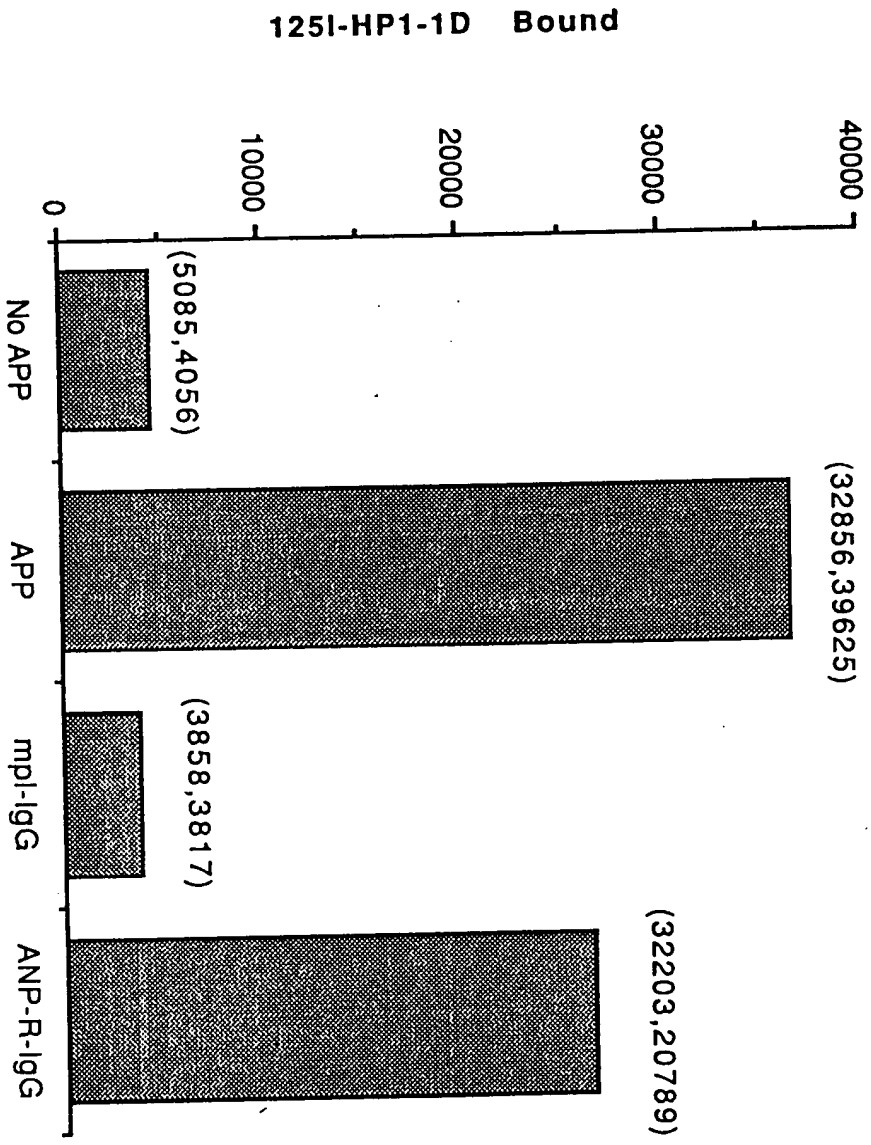

125I-HP1-1D Bound
0
10000
20000
30000
40000
No APP
(5085,4056)
APP
(32856,39625)
mpl-IgG
(3858,3817)
ANP-R-IgG
(32203,20789)

Figure 6

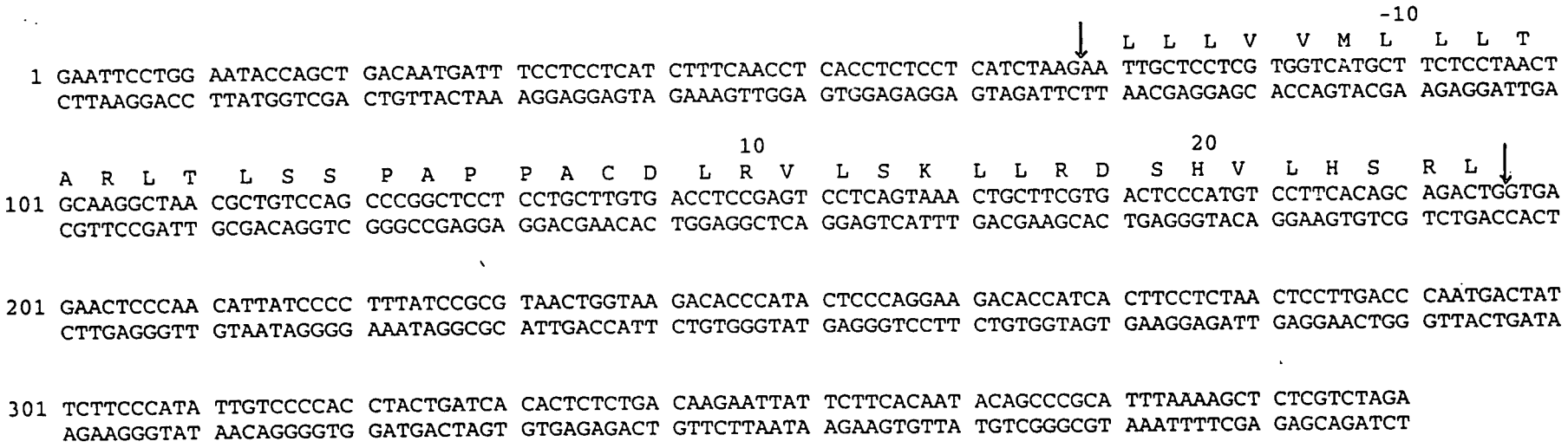
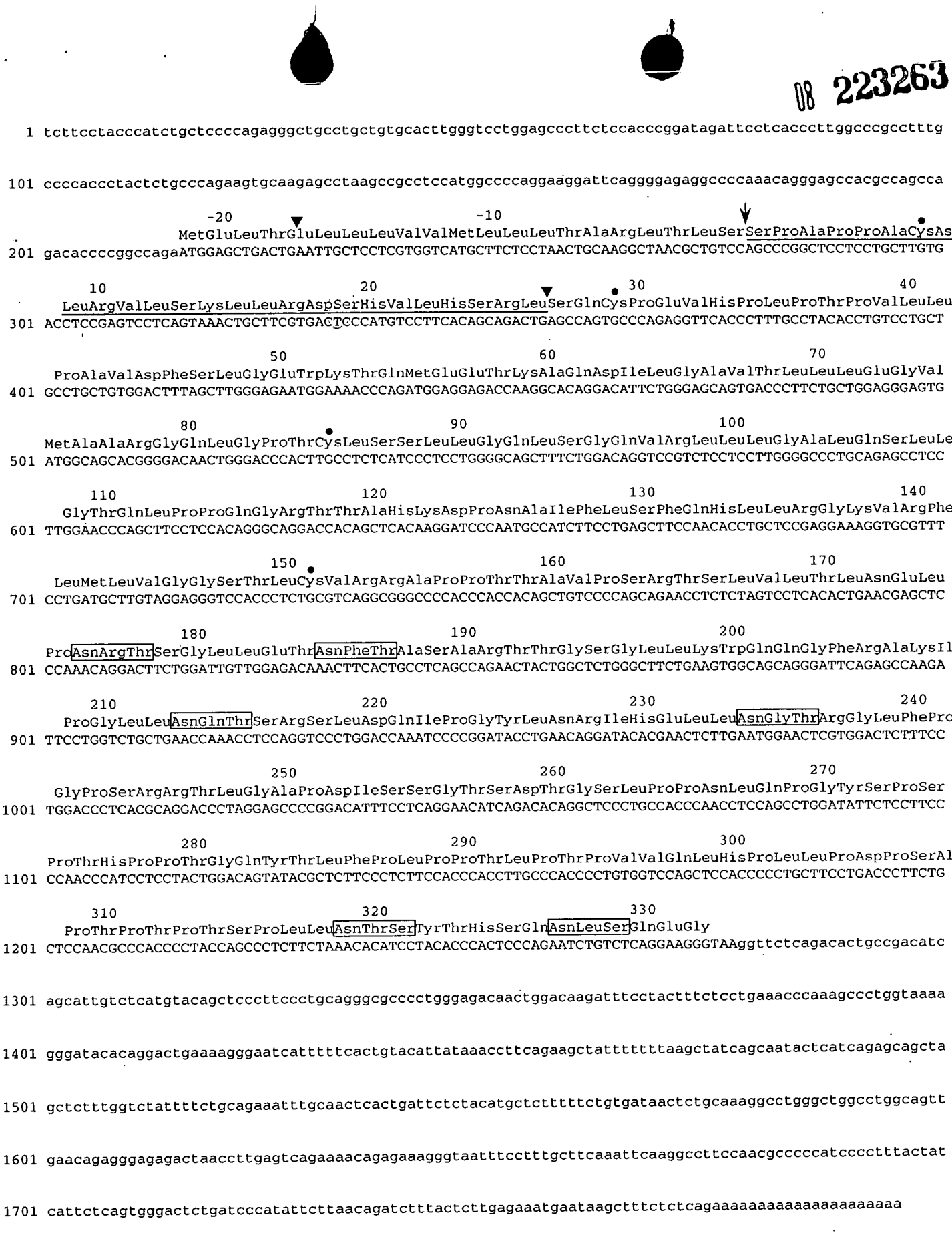


Figure 7

US 2003/0232963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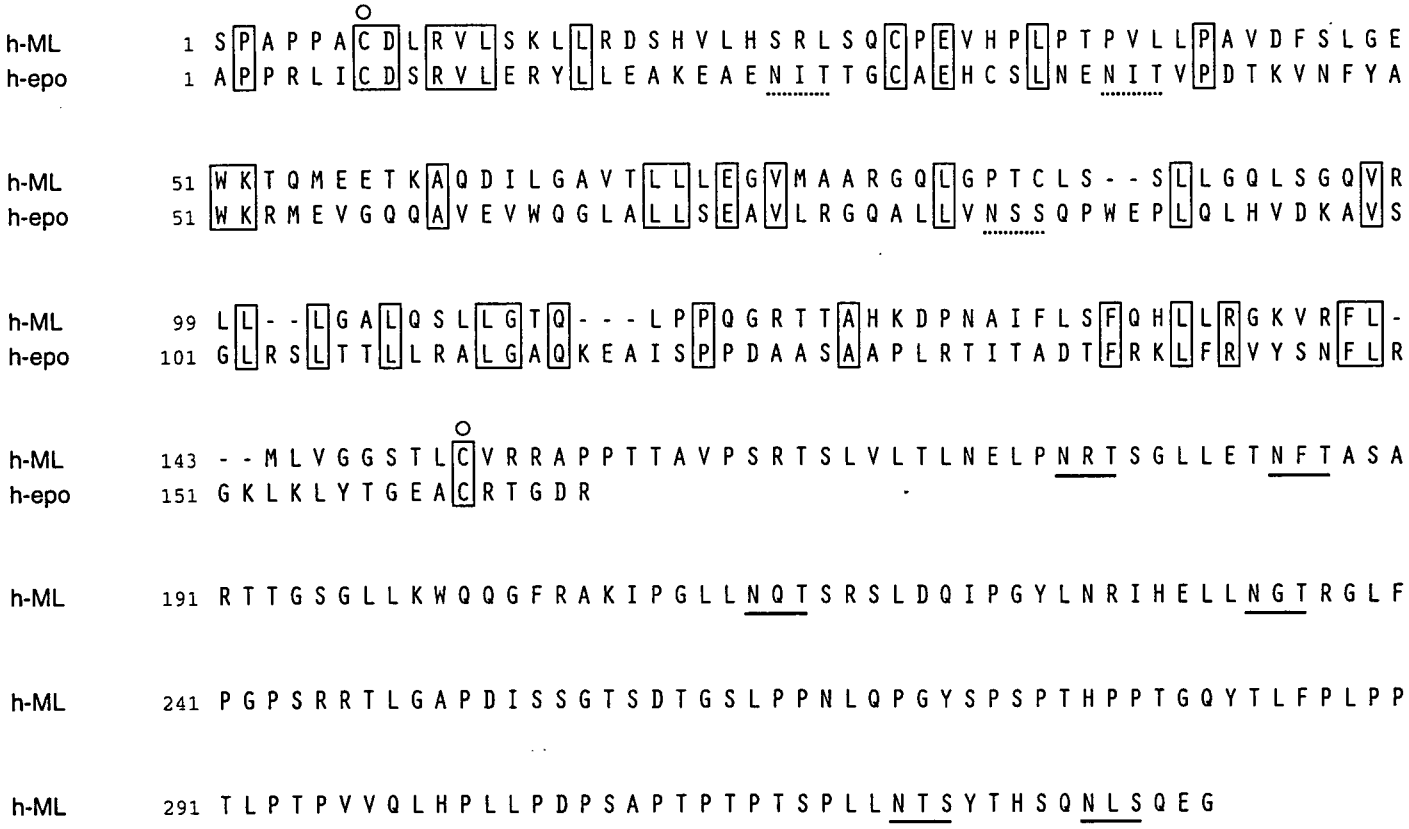
101 ccccaccctactctgcccagaagtgcaagagcctaagccgcctccatggccccaggaaggattcaggggagaggccccaaacagggagccacgccagcca
-20 -10
MetGluLeuThrGluLeuLeuLeuValValMetLeuLeuLeuThrAlaArgLeuThrLeuSerSerProAlaProProAlaCysAsp
201 gacaccccggccagaATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTGTCCAGCCCGGCTCCTCCTGCTTGTG
10 20 30 40
LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu
301 ACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCT
50 60 70
ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyVal
401 GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTG
80 90 100
MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
501 ATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCC
110 120 130 140
GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe
601 TTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTT
150 160 170
LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuAsnGluLeu
701 CCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGCGGGCCCCACCCACCACAGCTGTCCCCAGCAGAACCTCTCTAGTCCTCACACTGAACGAGCTC
180 190 200
ProAsnArgThrSerGlyLeuLeuGluThrAsnPheThrAlaSerAlaArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIle
801 CCAAACAGGACTTCTGGATTGTTGGAGACAAACTTCACTGCCTCAGCCAGAACTACTGGCTCTGGGCTTCTGAAGTGGCAGCAGGGATTCAGAGCCAAGA
210 220 230 240
ProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeuAsnArgIleHisGluLeuLeuAsnGlyThrArgGlyLeuPhePro
901 TTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTGGACCAAATCCCCGGATACCTGAACAGGATACACGAACTCTTGAATGGAACTCGTGGACTCTTTCC
250 260 270
GlyProSerArgArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyrSerProSer
1001 TGGACCCTCACGCAGGACCCTAGGAGCCCCGGACATTTCCTCAGGAACATCAGACACAGGCTCCCTGCCACCCAACCTCCAGCCTGGATATTCTCCTTCC
280 290 300
ProThrHisProProThrGlyGlnTyrThrLeuProLeuProProThrLeuProThrProValValGlnLeuHisProLeuLeuProAspProSerAla
1101 CCAACCCATCCTCCTACTGGACAGTATACGCTCTTCCCTCTTCCACCCACCTTGCCCACCCCTGTGGTCCAGCTCCACCCCCTGCTTCCTGACCCTTCTG
310 320 330
ProThrProThrProThrSerProLeuLeuAsnThrSerTyrThrHisSerGlnAsnLeuSerGlnGluGly
1201 CTCCAACGCCCACCCCTACCAGCCCTCTTCTAAACACATCCTACACCCACTCCCAGAATCTGTCTCAGGAAGGGTAAggttctcagacactgccgacatc
1301 agcattgtctcatgtacagctcccttccctgcagggcgcccctgggagacaactggacaagatttcctactttctcctgaaacccaaagccctggtaaaa
1401 gggatacacaggactgaaaagggaatcatttttcactgtacattataaaccttcagaagctatttttttaagctatcagcaatactcatcagagcagcta
1501 gctctttggtctattttctgcagaaatttgcaactcactgattctctacatgctctttttctgtgataactctgcaaaggcctgggctggcctggcagtt
1601 gaacagagggagagactaaccttgagtcagaaaacagagaaagggtaatttcctttgcttcaaattcaaggccttccaacgcccccatcccctttactat
1701 cattctcagtgggactctgatcccatattcttaacagatctttactcttgagaaatgaataagctttctctcagaaaaaaaaaaaaaaaaaaaaa

Figure 8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h-epo 1 A P P R L I C D S R V L E R Y L L E A K E A E N I T T G C A E H C S L N E N I T V P D T K V N F Y A
h-ML 51 W K T Q M E E T K A Q D I L G A V T L L L E G V M A A R G Q L G P T C L S - - S L L G Q L S G Q V R
h-epo 51 W K R M E V G Q Q A V E V W Q G L A L L S E A V L R G Q A L L V N S S Q P W E P L Q L H V D K A V S
h-ML 99 L L - - L G A L Q S L L G T Q - - - L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L -
h-epo 101 G L R S L T T L L R A L G A Q K E A I S P P D A A S A A P L R T I T A D T F R K L F R V Y S N F L R
h-ML 143 - - M L V G G S T L C V R R A P P T T A V P S R T S L V L T L N E L P N R T S G L L E T N F T A S A
h-epo 151 G K L K L Y T G E A C R T G D R
h-ML 191 R T T G S G L L K W Q Q G F R A K I P G L L N Q T S R S L D Q I P G Y L N R I H E L L N G T R G L F
h-ML 241 P G P S R R T L G A P D I S S G T S D T G S L P P N L Q P G Y S P S P T H P P T G Q Y T L F P L P P
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Figure 9

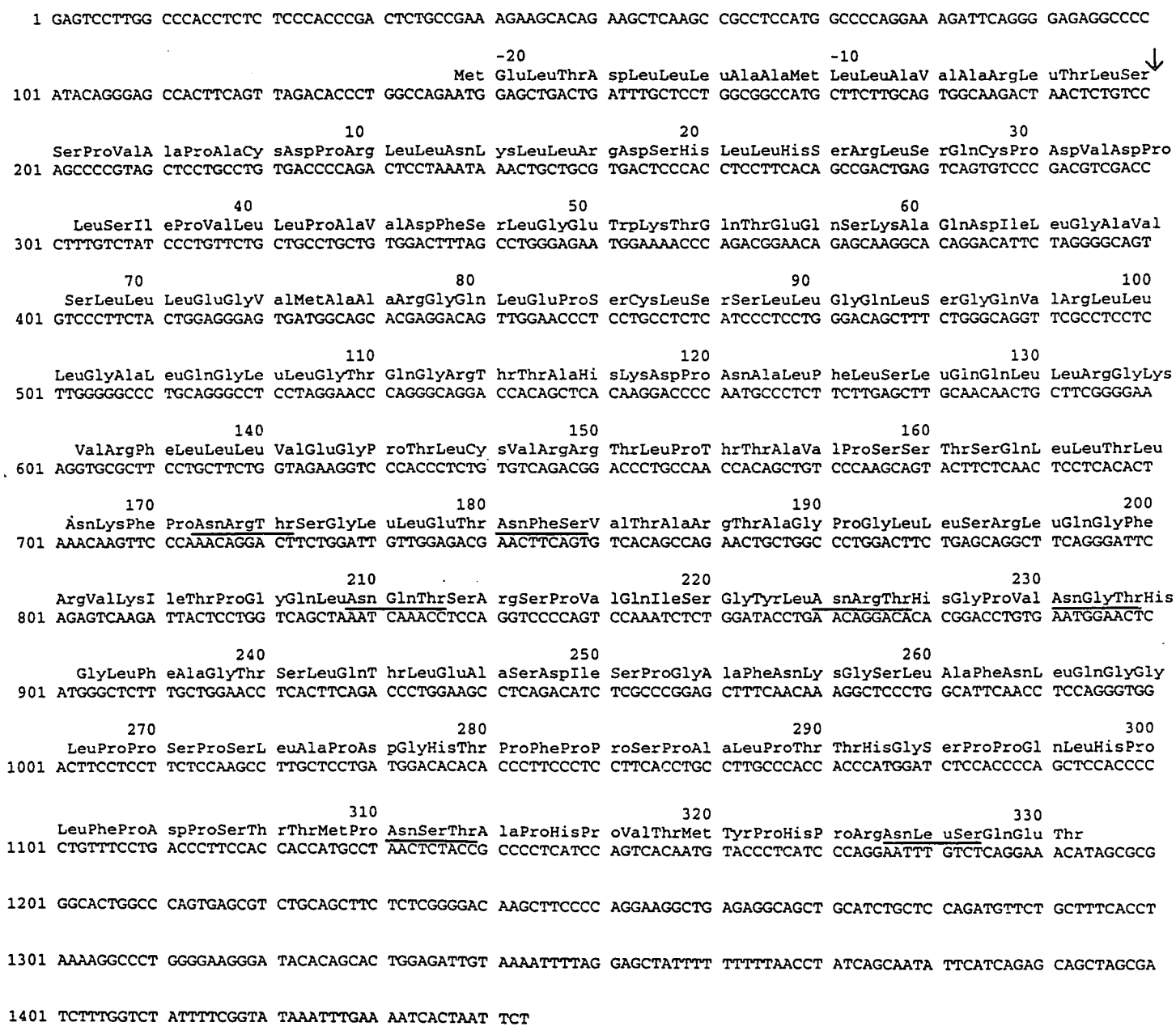
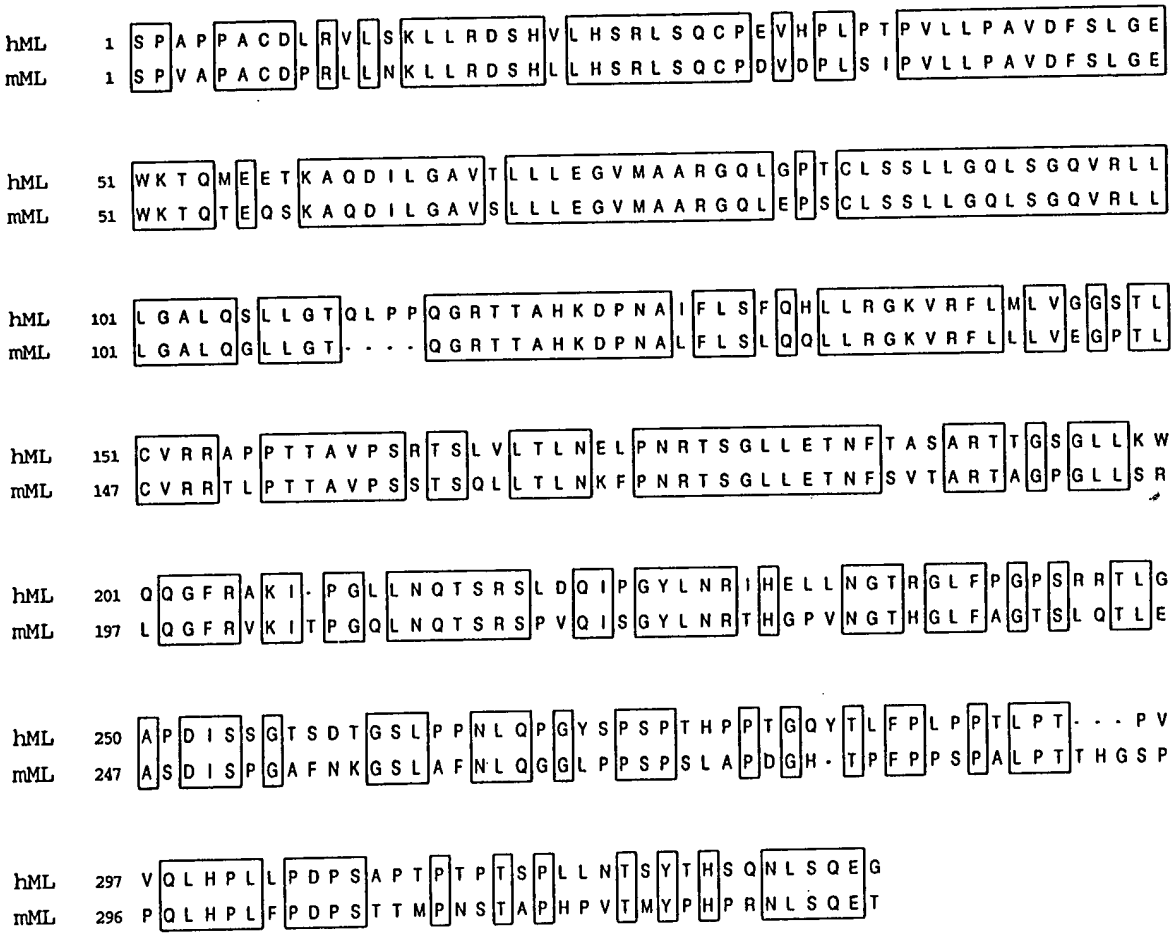


Figure 10

IL 223263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mML 51 WKTQTEQSKAQDILGAVSLLLEGVMAARGQLEPSCLSSLLGQLSGQVRLL
hML 101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
mML 101 LGALQGLLGT----QGRTTAHKDPNALFLSLQQLLRGKVRFLLLVEGPTL
hML 151 CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW
mML 147 CVRRTLPTTAVPSSTSQLLTLNKFPNRTSGLLETNFSVTARTAGPGLLSR
hML 201 QQGFRAKI·PGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLG
mML 197 LQGFRVKITPGQLNQTSRSPVQISGYLNRTHGPVNGTHGLFAGTSLQTLE
hML 250 APDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPT---PV
mML 247 ASDISPGAFNKGSLAFNLQGGLPPSPSLAPDGH·TPFPPSPALPTTHGSP
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Figure 11

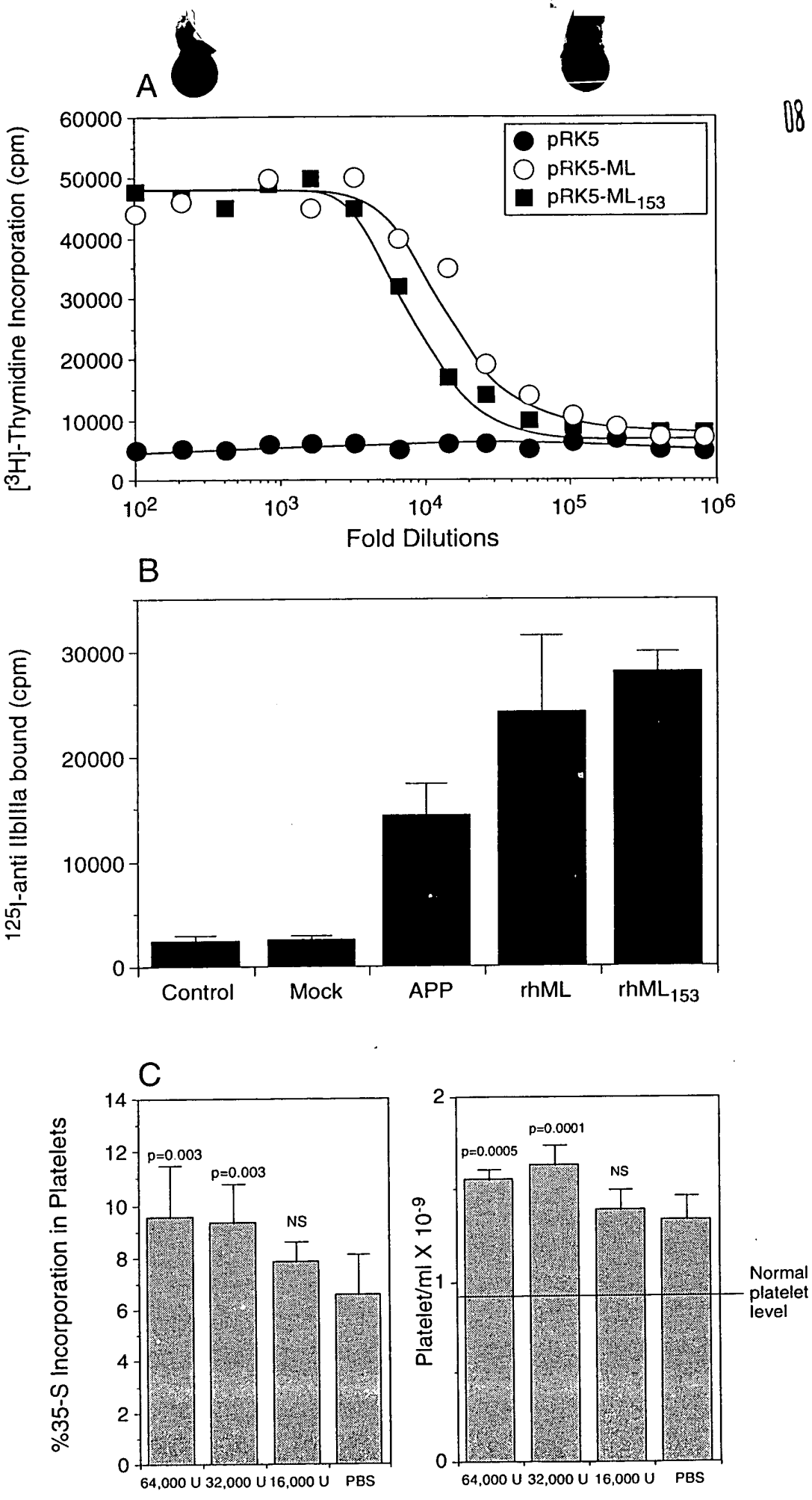
A
60000
50000
40000
30000
20000
10000
0
[3H]-Thymidine Incorporation (cpm)
pRK5
pRK5-ML
pRK5-ML153
10^2
10^3
10^4
10^5
10^6
Fold Dilutions
B
30000
20000
10000
0
125I-anti IIbIIIa bound (cpm)
Control
Mock
APP
rhML
rhML153
C
14
12
10
8
6
4
2
0
%35-S Incorporation in Platelets
p=0.003
p=0.003
NS
64,000 U
32,000 U
16,000 U
PBS
2
1
0
Platelet/ml X 10-9
p=0.0005
p=0.0001
NS
Normal platelet level
64,000 U
32,000 U
16,000 U
PBS

Figure 12